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The Government of the United States of America
as represented by the Secretary of the
Department of Health and Human Services

<130> 015280-382100PC

<141> 2001-05-29

<151> 1998-11-30

<151> 1999-11-24

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<170> PatentIn Ver. 2.1

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<223> MXR1

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tgcctccgag cgcacgcata ctgagatcct gagcctttgg ttaagaccga gctctattaa 180

gctgaaaaga taaaaactct ccag atg tct tcc agt aat gtc gaa gtt ttt 231

Met Ser Ser Ser Asn Val Glu Val Phe

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atc cca qtq tca caa gga aac acc aat ggc ttc ccc gcg aca gtt tcc 279

Ile Pro Val Ser Gln Gly Asn Thr Asn Gly Phe Pro Ala Thr Val Ser

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aat gac ctg aag gca ttt act gaa gga gct gtg tta agt ttt cat aac 327

Asn Asp Leu Lys Ala Phe Thr Glu Gly Ala Val Leu Ser Phe His Asn

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atc tgc tat cga qta aaa ctg aag agt ggc ttt cta cct tgt cga aaa 375

Ile Cys Tyr Arg Val Lys Leu Lys Ser Gly Phe Leu Pro Cys Arg Lys

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| cca gtt gag aaa gaa ata tta tcg aat atc aat ggg atc atg aaa cct | 423 |
| Pro Val Glu Lys Glu Ile Leu Ser Asn Ile Asn Gly Ile Met Lys Pro | |
| 60 65 70 | |
| ggt ctc aac gcc atc ctg gga ccc aca ggt gga ggc aaa tct tcg tta | 471 |
| Gly Leu Asn Ala Ile Leu Gly Pro Thr Gly Gly Gly Lys Ser Ser Leu | |
| 75 80 85 | |
| tta gat gtc tta gct gca agg aaa gat cca agt gga tta tct gga gat | 519 |
| Leu Asp Val Leu Ala Ala Arg Lys Asp Pro Ser Gly Leu Ser Gly Asp | |
| 90 95 100 105 | |
| gtt ctg ata aat gga gca ccg cga cct gcc aat ttc aaa tgt aat tca | 567 |
| Val Leu Ile Asn Gly Ala Pro Arg Pro Ala Asn Phe Lys Cys Asn Ser | |
| 110 115 120 | |
| ggt tac gtg gta caa gat gat gtt gtg atg ggc act ctg acg gtg aga | 615 |
| Gly Tyr Val Val Gln Asp Asp Val Val Met Gly Thr Leu Thr Val Arg | |
| 125 130 135 | |
| gaa aac tta cag ttc tca gca gct ctt cgg ctt gca aca act atg acg | 663 |
| Glu Asn Leu Gln Phe Ser Ala Ala Leu Arg Leu Ala Thr Thr Met Thr | |
| 140 145 150 | |
| aat cat gaa aaa aac gaa cgg att aac agg gtc att gaa gag tta ggt | 711 |
| Asn His Glu Lys Asn Glu Arg Ile Asn Arg Val Ile Glu Glu Leu Gly | |
| 155 160 165 | |
| ctg gat aaa gtg gca gac tcc aag gtt gga act cag ttt atc cgt ggt | 759 |
| Leu Asp Lys Val Ala Asp Ser Lys Val Gly Thr Gln Phe Ile Arg Gly | |
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| gtg tct gga gga gaa aga aaa agg act agt ata gga atg gag ctt atc | 807 |
| Val Ser Gly Gly Glu Arg Lys Arg Thr Ser Ile Gly Met Glu Leu Ile | |
| 190 195 200 | |
| act gat cct tcc atc ttg tcc ttg gat gag cct aca act ggc tta gac | 855 |
| Thr Asp Pro Ser Ile Leu Ser Leu Asp Glu Pro Thr Thr Gly Leu Asp | |
| 205 210 215 | |
| tca agc aca gca aat gct gtc ctt ttg ctc ctg aaa agg atg tct aag | 903 |
| Ser Ser Thr Ala Asn Ala Val Leu Leu Leu Leu Lys Arg Met Ser Lys | |
| 220 225 230 | |
| cag gga cga aca atc atc ttc tcc att cat cag cct cga tat tcc atc | 951 |
| Gln Gly Arg Thr Ile Ile Phe Ser Ile His Gln Pro Arg Tyr Ser Ile | |
| 235 240 245 | |
| ttc aag ttg ttt gat agc ctc acc tta ttg gcc tca gga aga ctt atg | 999 |
| Phe Lys Leu Phe Asp Ser Leu Thr Leu Leu Ala Ser Gly Arg Leu Met | |
| 250 255 260 265 | |
| ttc cac ggg cct gct cag gag gcc ttg gga tac ttt gaa tca gct ggt | 1047 |
| Phe His Gly Pro Ala Gln Glu Ala Leu Gly Tyr Phe Glu Ser Ala Gly | |
| 270 275 280 | |
| tat cac tgt gag gcc tat aat aac cct gca gac ttc ttc ttg gac atc | 1095 |
| Tyr His Cys Glu Ala Tyr Asn Asn Pro Ala Asp Phe Phe Leu Asp Ile | |
| 285 290 295 | |

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| att aat gga gat tcc act gct gtg gca tta aac aga gaa gaa gac ttt | 1143 |
| Ile Asn Gly Asp Ser Thr Ala Val Ala Leu Asn Arg Glu Glu Asp Phe | |
| 300 305 310 | |
| aaa gcc aca gag atc ata gag cct tcc aag cag gat aag cca ctc ata | 1191 |
| Lys Ala Thr Glu Ile Ile Glu Pro Ser Lys Gln Asp Lys Pro Leu Ile | |
| 315 320 325 | |
| gaa aaa tta gcg gag att tat gtc aac tcc tcc ttc tac aaa gag aca | 1239 |
| Glu Lys Leu Ala Glu Ile Tyr Val Asn Ser Ser Phe Tyr Lys Glu Thr | |
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| aaa gct gaa tta cat caa ctt tcc ggg ggt gag aag aag aag aag atc | 1287 |
| Lys Ala Glu Leu His Gln Leu Ser Gly Gly Glu Lys Lys Lys Lys Ile | |
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| aca gtc ttc aag gag atc agc tac acc acc tcc ttc tgt cat caa ctc | 1335 |
| Thr Val Phe Lys Glu Ile Ser Tyr Thr Thr Ser Phe Cys His Gln Leu | |
| 365 370 375 | |
| aga tgg gtt tcc aag cgt tca ttc aaa aac ttg ctg ggt aat ccc cag | 1383 |
| Arg Trp Val Ser Lys Arg Ser Phe Lys Asn Leu Leu Gly Asn Pro Gln | |
| 380 385 390 | |
| gcc tct ata gct cag atc att gtc aca gtc gta ctg gga ctg gtt ata | 1431 |
| Ala Ser Ile Ala Gln Ile Ile Val Thr Val Val Leu Gly Leu Val Ile | |
| 395 400 405 | |
| ggg gcc att tac ttt ggg cta aaa aat gat tct act gga atc cag aac | 1479 |
| Gly Ala Ile Tyr Phe Gly Leu Lys Asn Asp Ser Thr Gly Ile Gln Asn | |
| 410 415 420 425 | |
| aga gct ggg gtt ctc ttc ttc ctg acg acc aac cag tgt ttc agc agt | 1527 |
| Arg Ala Gly Val Leu Phe Phe Leu Thr Thr Asn Gln Cys Phe Ser Ser | |
| 430 435 440 | |
| gtt tca gcc gtg gaa ctc ttt gtg gta gag aag aag ctc ttc ata cat | 1575 |
| Val Ser Ala Val Glu Leu Phe Val Val Glu Lys Lys Leu Phe Ile His | |
| 445 450 455 | |
| gaa tac atc agc gga tac tac aga gtg tca tct tat ttc ctt gga aaa | 1623 |
| Glu Tyr Ile Ser Gly Tyr Tyr Arg Val Ser Ser Tyr Phe Leu Gly Lys | |
| 460 465 470 | |
| ctg tta tct gat tta tta ccc atg agg atg tta cca agt att ata ttt | 1671 |
| Leu Leu Ser Asp Leu Leu Pro Met Arg Met Leu Pro Ser Ile Ile Phe | |
| 475 480 485 | |
| acc tgt ata gtg tac ttc atg tta gga ttg aag cca aag gca gat gcc | 1719 |
| Thr Cys Ile Val Tyr Phe Met Leu Gly Leu Lys Pro Lys Ala Asp Ala | |
| 490 495 500 505 | |
| ttc ttc gtt atg atg ttt acc ctt atg atg gtg gct tat tca gcc agt | 1767 |
| Phe Phe Val Met Met Phe Thr Leu Met Met Val Ala Tyr Ser Ala Ser | |
| 510 515 520 | |
| tcc atg gca ctg gcc ata gca gca ggt cag agt gtg gtt tct gta gca | 1815 |
| Ser Met Ala Leu Ala Ile Ala Ala Gly Gln Ser Val Val Ser Val Ala | |
| 525 530 535 | |

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aca ctt ctc atg acc atc tgt ttt gtg ttt atg atg att ttt tca ggt 1863
 Thr Leu Leu Met Thr Ile Cys Phe Val Phe Met Met Ile Phe Ser Gly
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ctg ttg gtc aat ctc aca acc att gca tct tgg ctg tca tgg ctt cag 1911
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 555 560 565

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 570 575 580 585

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cct tgt aac tat gca aca tgt act ggc gaa gaa tat ttg gta aag cag 2055
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gct tgt atg att gtt att ttc ctc aca att gcc tac ctg aaa ttg tta 2151
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 635 640 645

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aaatcacaac aaactgaatt aaacatgaaa gaaccacaaga catcatgtat cgcataattag 2379

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aggagaattg aattctggaa actcctgaca agttattact gtctctggca tttgtttctt 2499

catcttttaa atgaataggt aggttagtag cccttcagtc ttaatacttt atgatgctat 2559

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<213> Homo sapiens

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 Lys Ser Gly Phe Leu Pro Cys Arg Lys Pro Val Glu Lys Glu Ile Leu
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 Ser Asn Ile Asn Gly Ile Met Lys Pro Gly Leu Asn Ala Ile Leu Gly
 65 70 75 80
 Pro Thr Gly Gly Gly Lys Ser Ser Leu Leu Asp Val Leu Ala Ala Arg
 85 90 95
 Lys Asp Pro Ser Gly Leu Ser Gly Asp Val Leu Ile Asn Gly Ala Pro
 100 105 110
 Arg Pro Ala Asn Phe Lys Cys Asn Ser Gly Tyr Val Val Gln Asp Asp
 115 120 125
 Val Val Met Gly Thr Leu Thr Val Arg Glu Asn Leu Gln Phe Ser Ala
 130 135 140
 Ala Leu Arg Leu Ala Thr Thr Met Thr Asn His Glu Lys Asn Glu Arg
 145 150 155 160
 Ile Asn Arg Val Ile Glu Glu Leu Gly Leu Asp Lys Val Ala Asp Ser
 165 170 175
 Lys Val Gly Thr Gln Phe Ile Arg Gly Val Ser Gly Gly Glu Arg Lys
 180 185 190
 Arg Thr Ser Ile Gly Met Glu Leu Ile Thr Asp Pro Ser Ile Leu Ser
 195 200 205
 Leu Asp Glu Pro Thr Thr Gly Leu Asp Ser Ser Thr Ala Asn Ala Val
 210 215 220
 Leu Leu Leu Leu Lys Arg Met Ser Lys Gln Gly Arg Thr Ile Ile Phe
 225 230 235 240
 Ser Ile His Gln Pro Arg Tyr Ser Ile Phe Lys Leu Phe Asp Ser Leu
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 Thr Leu Leu Ala Ser Gly Arg Leu Met Phe His Gly Pro Ala Gln Glu
 260 265 270
 Ala Leu Gly Tyr Phe Glu Ser Ala Gly Tyr His Cys Glu Ala Tyr Asn
 275 280 285
 Asn Pro Ala Asp Phe Phe Leu Asp Ile Ile Asn Gly Asp Ser Thr Ala
 290 295 300
 Val Ala Leu Asn Arg Glu Glu Asp Phe Lys Ala Thr Glu Ile Ile Glu
 305 310 315 320
 Pro Ser Lys Gln Asp Lys Pro Leu Ile Glu Lys Leu Ala Glu Ile Tyr
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Val Asn Ser Ser Phe Tyr Lys Glu Thr Lys Ala Glu Leu His Gln Leu
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 Tyr Thr Thr Ser Phe Cys His Gln Leu Arg Trp Val Ser Lys Arg Ser
 370 375 380
 Phe Lys Asn Leu Leu Gly Asn Pro Gln Ala Ser Ile Ala Gln Ile Ile
 385 390 395 400
 Val Thr Val Val Leu Gly Leu Val Ile Gly Ala Ile Tyr Phe Gly Leu
 405 410 415
 Lys Asn Asp Ser Thr Gly Ile Gln Asn Arg Ala Gly Val Leu Phe Phe
 420 425 430
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 Val Val Glu Lys Lys Leu Phe Ile His Glu Tyr Ile Ser Gly Tyr Tyr
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 Arg Val Ser Ser Tyr Phe Leu Gly Lys Leu Leu Ser Asp Leu Leu Pro
 465 470 475 480
 Met Arg Met Leu Pro Ser Ile Ile Phe Thr Cys Ile Val Tyr Phe Met
 485 490 495
 Leu Gly Leu Lys Pro Lys Ala Asp Ala Phe Phe Val Met Met Phe Thr
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 Leu Met Met Val Ala Tyr Ser Ala Ser Ser Met Ala Leu Ala Ile Ala
 515 520 525
 Ala Gly Gln Ser Val Val Ser Val Ala Thr Leu Leu Met Thr Ile Cys
 530 535 540
 Phe Val Phe Met Met Ile Phe Ser Gly Leu Leu Val Asn Leu Thr Thr
 545 550 555 560
 Ile Ala Ser Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro Arg Tyr
 565 570 575
 Gly Phe Thr Ala Leu Gln His Asn Glu Phe Leu Gly Gln Asn Phe Cys
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 Pro Gly Leu Asn Ala Thr Gly Asn Asn Pro Cys Asn Tyr Ala Thr Cys
 595 600 605
 Thr Gly Glu Glu Tyr Leu Val Lys Gln Gly Ile Asp Leu Ser Pro Trp
 610 615 620
 Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met Ile Val Ile Phe
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 Ile Ala Thr Gly Gln Ser Val Val Ser Val Ala Thr Leu Leu Met Thr
 20 25 30
 atc gct ttt gta ttt atg atg ctc ttt tct ggc ctc ttg gtg aat ctc 144
 Ile Ala Phe Val Phe Met Met Leu Phe Ser Gly Leu Leu Val Asn Leu
 35 40 45
 aga acc att ggg cct tgg ctg tcc tgg ctt cag tac ttt agc att cct 192
 Arg Thr Ile Gly Pro Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro
 50 55 60
 cga tat ggc ttc aca gct ttg cag tat aat gaa ttc ttg gga caa gag 240
 Arg Tyr Gly Phe Thr Ala Leu Gln Tyr Asn Glu Phe Leu Gly Gln Glu
 65 70 75 80
 ttt tgt cca gga ttc aat gta acg gac aac agc act tgt gtt aac agc 288
 Phe Cys Pro Gly Phe Asn Val Thr Asp Asn Ser Thr Cys Val Asn Ser
 85 90 95
 tat gca ata tgt act ggt aac gag tac ttg ata aat cag ggc atc gaa 336
 Tyr Ala Ile Cys Thr Gly Asn Glu Tyr Leu Ile Asn Gln Gly Ile Glu
 100 105 110
 ctg tca cct tgg gga ctg tgg aag aat cat gtg gcc ctg gct tgt atg 384
 Leu Ser Pro Trp Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met
 115 120 125
 att att atc ttc ctc aca att gcc tac ctg aaa ttg ttg ttt ctt aaa 432
 Ile Ile Ile Phe Leu Thr Ile Ala Tyr Leu Lys Leu Leu Phe Leu Lys
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09856927.091901

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 35 40 45

Arg Thr Ile Gly Pro Trp Leu Ser Trp Leu Gln Tyr Phe Ser Ile Pro
 50 55 60

Arg Tyr Gly Phe Thr Ala Leu Gln Tyr Asn Glu Phe Leu Gly Gln Glu
 65 70 75 80

Phe Cys Pro Gly Phe Asn Val Thr Asp Asn Ser Thr Cys Val Asn Ser
 85 90 95

Tyr Ala Ile Cys Thr Gly Asn Glu Tyr Leu Ile Asn Gln Gly Ile Glu
 100 105 110

Leu Ser Pro Trp Gly Leu Trp Lys Asn His Val Ala Leu Ala Cys Met
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Lys Tyr Ser
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<213> Artificial Sequence

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